```
AGCATCCTGA GTAATGAGTG GCCTGGGCCG GAGCAGGCGA GGTGGCCGGA GCCGTGTGGA    60
CCAGGAGGAG CGCTTTCCAC AGGGCCTGTG GACGGGGGTG GCTATGAGAT CCTGCCCCGA   120
AGAGCAGTAC TGGGATCCTC TGCTGGGTAC CTGCATGTCC TGCAAAACCA TTTGCAACCA   180
TCAGAGCCAG CGCACCTGTG CAGCCTTCTG CAGGTCACTC AGCTGCCGCA AGGAGCAACG   240
CAAGTTCTAT GACCATCTCC TGAGGGACTG CATCAGCTGT GCCTCCATCT GTGGACAGCA   300
CCCTAAGCAA TGTGCATACT TCTGTGAGAA CAAGCTCAGG AGCCCAGTGA ACCTTCCACC   360
AGAGCTCAGG AGACAGCGGA GTGGAGAAGT TGAAAACAAT TCAGACAACT CGGGAAGGTA   420
CCAAGGATTG GAGCACAGAG GCTCAGAAGC AAGTCCAGCT CTCCCGGGGC TGAAGCTGAG   480
TGCAGATCAG GTGGCCCTGG TCTACAGCAC GCTGGGGCTC TGCCTGTGTG CCGTCCTCTG   540
CTGCTTCCTG GTGGCGGTGG CCTGCTTCCT CAAGAAGAGG GGGGATCCCT GCTCCTGCCA   600
GCCCCGCTCA AGGCCCCGTC AAAGTCCGGC CAAGTCTTCC CAGGATCACG CGATGGAAGC   660
CGGCAGCCCT GTGAGCACAT CCCCCGAGCC AGTGGAGACC TGCAGCTTCT GCTTCCCTGA   720
GTGCAGGGCG CCCACGCAGG AGAGCGCAGT CACGCCTGGG ACCCCCGACC CCACTTGTGC   780
TGGAAGGTGG GGGTGCCACA CCAGGACCAC AGTCCTGCAG CCTTGCCCAC ACATCCCAGA   840
CAGTGGCCTT GGCATTGTGT GTGTGCCTGC CCAGGAGGGG GGCCCAGGTG CATAAATGGG   900
GGTCAGGGAG GGAAAGGAGG AGGGAGAGAG ATGGAGAGGA GGGGAGAGAG AAAGAGAGGT   960
GGGGAGAGGG GAGAGAGATA TGAGGAGAGA GAGACAGAGG AGGCAGAAAG GGAGAGAAAC  1020
AGAGGAGACA GAGAGGGAGA GAGAGACAGA GGGAGAGAGA GACAGAGGGG AAGAGAGGCA  1080
GAGAGGGAAA GAGGCAGAGA AGGAAAGAGA CAGGCAGAGA AGGAGAGAGG CAGAGAGGGA  1140
GAGAGGCAGA GAGGGAGAGA GGCAGAGAGA CAGAGAGGGA GAGAGGGACA GAGAGAGATA  1200
GAGCAGGAGG TCGGGGCACT CTGAGTCCCA GTTCCCAGTG CAGCTGTAGG TCGTCATCAC  1260
CTAACCACAC GTGCAATAAA GTCCTCGTGC CTGCTGCTCA CAGCCCCCGA GAGCCCCTCC  1320
TCCTGGAGAA TAAAACCTTT GGCAGCTGCC CTTCCTCAAA AAAAAAAAAA AAAAAAA     1377
```

FIGURE 1A

Met	Ser	Gly	Leu	Gly	Arg	Ser	Arg	Arg	Gly	Gly	Arg	Ser	Arg	Val	Asp
1				5					10					15	
Gln	Glu	Glu	Arg	Phe	Pro	Gln	Gly	Leu	Trp	Thr	Gly	Val	Ala	Met	Arg
			20					25					30		
Ser	Cys	Pro	Glu	Glu	Gln	Tyr	Trp	Asp	Pro	Leu	Leu	Gly	Thr	Cys	Met
		35					40					45			
Ser	Cys	Lys	Thr	Ile	Cys	Asn	His	Gln	Ser	Gln	Arg	Thr	Cys	Ala	Ala
	50					55					60				
Phe	Cys	Arg	Ser	Leu	Ser	Cys	Arg	Lys	Glu	Gln	Gly	Lys	Phe	Tyr	Asp
65					70					75					80
His	Leu	Leu	Arg	Asp	Cys	Ile	Ser	Cys	Ala	Ser	Ile	Cys	Gly	Gln	His
				85					90					95	
Pro	Lys	Gln	Cys	Ala	Tyr	Phe	Cys	Glu	Asn	Lys	Leu	Arg	Ser	Pro	Val
			100					105					110		
Asn	Leu	Pro	Pro	Glu	Leu	Arg	Arg	Gln	Arg	Ser	Gly	Glu	Val	Glu	Asn
		115					120					125			
Asn	Ser	Asp	Asn	Ser	Gly	Arg	Tyr	Gln	Gly	Leu	Glu	His	Arg	Gly	Ser
	130					135					140				
Glu	Ala	Ser	Pro	Ala	Leu	Pro	Gly	Leu	Lys	Leu	Ser	Ala	Asp	Gln	Val
145					150					155					160
Ala	Leu	Val	Tyr	Ser	Thr	Leu	Gly	Leu	Cys	Leu	Cys	Ala	Val	Leu	Cys
				165					170					175	
Cys	Phe	Leu	Val	Ala	Val	Ala	Cys	Phe	Leu	Lys	Lys	Arg	Gly	Asp	Pro
			180					185					190		
Cys	Ser	Cys	Gln	Pro	Arg	Ser	Arg	Pro	Arg	Gln	Ser	Pro	Ala	Lys	Ser
		195					200					205			
Ser	Gln	Asp	His	Ala	Met	Glu	Ala	Gly	Ser	Pro	Val	Ser	Thr	Ser	Pro
	210					215					220				
Glu	Pro	Val	Glu	Thr	Cys	Ser	Phe	Cys	Phe	Pro	Glu	Cys	Arg	Ala	Pro
225					230					235					240
Thr	Gln	Glu	Ser	Ala	Val	Thr	Pro	Gly	Thr	Pro	Asp	Pro	Thr	Cys	Ala
				245					250					255	
Gly	Arg	Trp	Gly	Cys	His	Thr	Arg	Thr	Thr	Val	Leu	Gln	Pro	Cys	Pro
			260					265					270		
His	Ile	Pro	Asp	Ser	Gly	Leu	Gly	Ile	Val	Cys	Val	Pro	Ala	Gln	Glu
		275					280					285			
Gly	Gly	Pro	Gly	Ala											
	290														

FIGURE 1B

AGCAAGTTCA GCCTGGTTAA GTCCAAGCTG AATTCCGGTC AAAGTTCAAG
TAGTGATATG GATGACTCCA CAGAAAGGGA GCAGTCACGC CTTACTTCTT
GCCTTAAGAA AAGAGAAGAA ATGAAACTGA AGGAGTGTGT TTCCATCCTC
CCACGGAAGG AAAGCCCCTC TGTCCGATCC TCCAAAGACG GAAAGCTGCT
GGCTGCAACC TTGCTGCTGG CACTGCTGTC TTGCTGCCTC ACGGTGGTGT
CTTTCTACCA GGTGGCCGCC CTGCAAGGGG ACCTGGCCAG CCTCCGGGCA
GAGCTGCAGG GCCACCACGC GGAGAAGCTG CCAGCAGGAG CAGGAGCCCC
CAAGGCCGGC CTGGAGGAAG CTCCAGCTGT CACCGCGGGA CTGAAAATCT
TTGAACCACC AGCTCCAGGA GAAGGCAACT CCAGTCAGAA CAGCAGAAAT
AAGCGTGCCG TTCAGGGTCC AGAAGAAACA GTCACTCAAG ACTGCTTGCA
ACTGATTGCA GACAGTGAAA CACCAACTAT ACAAAAAGGA TCTTACACAT
TTGTTCCATG GCTTCTCAGC TTTAAAAGGG GAAGTGCCCT AGAAGAAAAA
GAGAATAAAA TATTGGTCAA AGAAACTGGT TACTTTTTTA TATATGGTCA
GGTTTTATAT ACTGATAAGA CCTACGCCAT GGGACATCTA ATTCAGAGGA
AGAAGGTCCA TGTCTTTGGG GATGAATTGA GTCTGGTGAC TTTGTTTCGA
TGTATTCAAA ATATGCCTGA AACACTACCC AATAATTCCT GCTATTCAGC
TGGCATTGCA AAACTGGAAG AAGGAGATGA ACTCCAACTT GCAATACCAA
GAGAAAATGC ACAAATATCA CTGGATGGAG ATGTCACATT TTTTGGTGCA
TTGAAACTGC TGTGACCTAC TTACACCATG TCTGTAGCTA TTTTCCTCCC
TTTCTCTGTA CCTCTAAGAA GAAAGAATCT AACTGAAAAT ACCAAAAAAA
AAAAAAAAAA AAAAAGATCT TTAATTAAGC GGCCGCAAGC TTATTCCCTT
TAGTGAG

FIGURE 2A

MDDSTEREQS RLTSCLKKRE EMKLKECVSI LPRKESPSVR SSKDGKLLAA
TLLLALLSCC LTVVSFYQVA ALQGDLASLR AELQGHHAEK LPAGAGAPKA
GLEEAPAVTA GLKIFEPPAP GEGNSSQNSR NKRAVQGPEE TVTQDCLQLI
ADSETPTIQK GSYTFVPWLL SFKRGSALEE KENKILVKET GYFFIYGQVL
YTDKTYAMGH LIQRKKVHVF GDELSLVTLF RCIQNMPETL PNNSCYSAGI
AKLEEGDELQ LAIPRENAQI SLDGDVTFFG ALKLL

FIGURE 2B

MARRLWILSL LAVTLTVALA APSQKSKRRT SSDRMKQIED KIEEILSKIY
HIENEIARIK KLIGERTRSG NSSQNSRNKR AVQGPEETVT QDCLQLIADS
ETPTIQKGSY TFVPWLLSFK RGSALEEKEN KILVKETGYF FIYGQVLYTD
KTYAMGHLIQ RKKVHVFGDE LSLVTLFRCI QNMPETLPNN SCYSAGIAKL
EEGDELQLAI PRENAQISLD GDVTFFGALK LL
(SEQ ID NO:3)

FIGURE 3

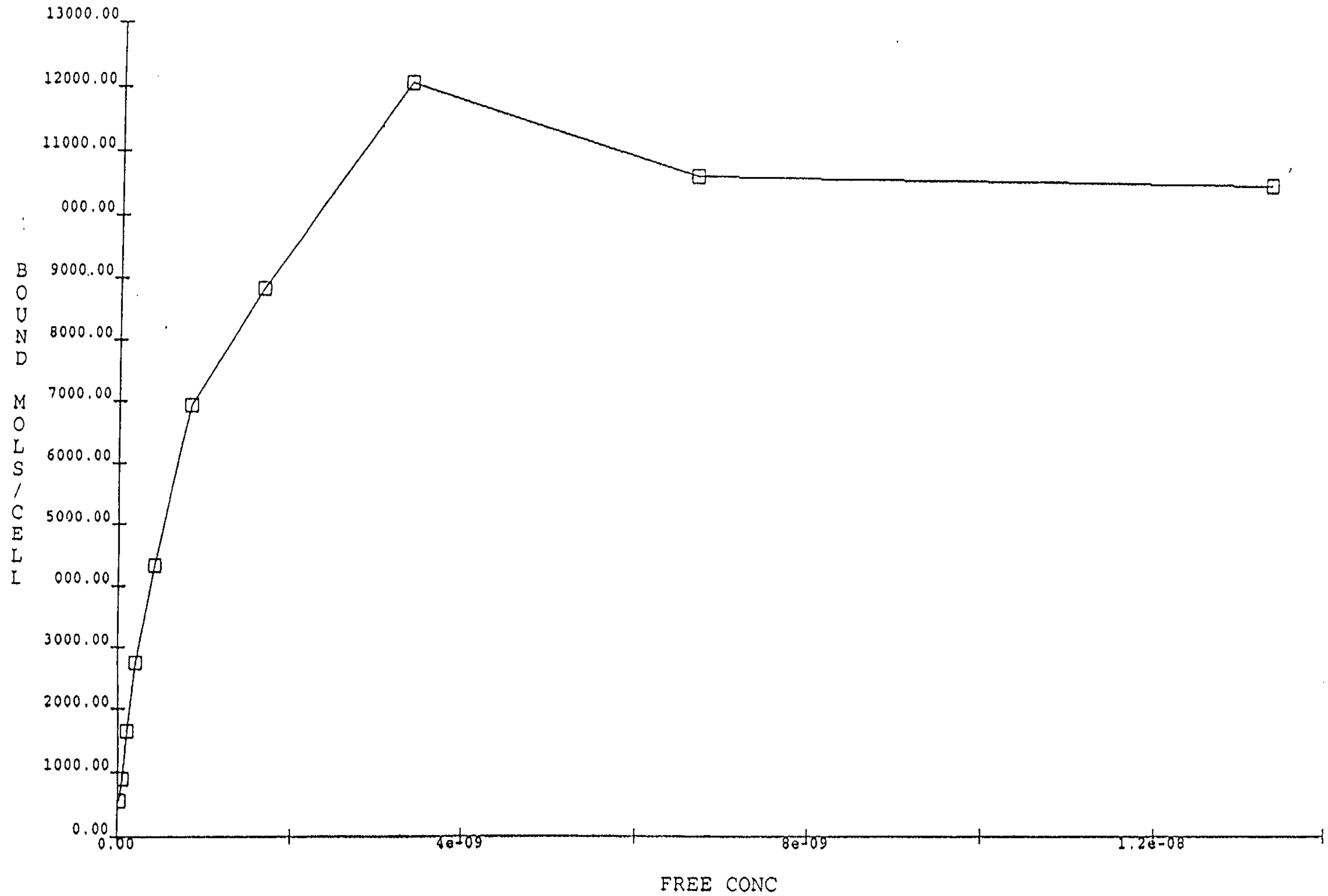

13000.00
12000.00
11000.00
000.00
9000.00
8000.00
7000.00
6000.00
5000.00
000.00
3000.00
2000.00
1000.00
0.00
BOUND MOLS/CELL
0.00
4e-09
8e-09
1.2e-08
FREE CONC

Figure 4A

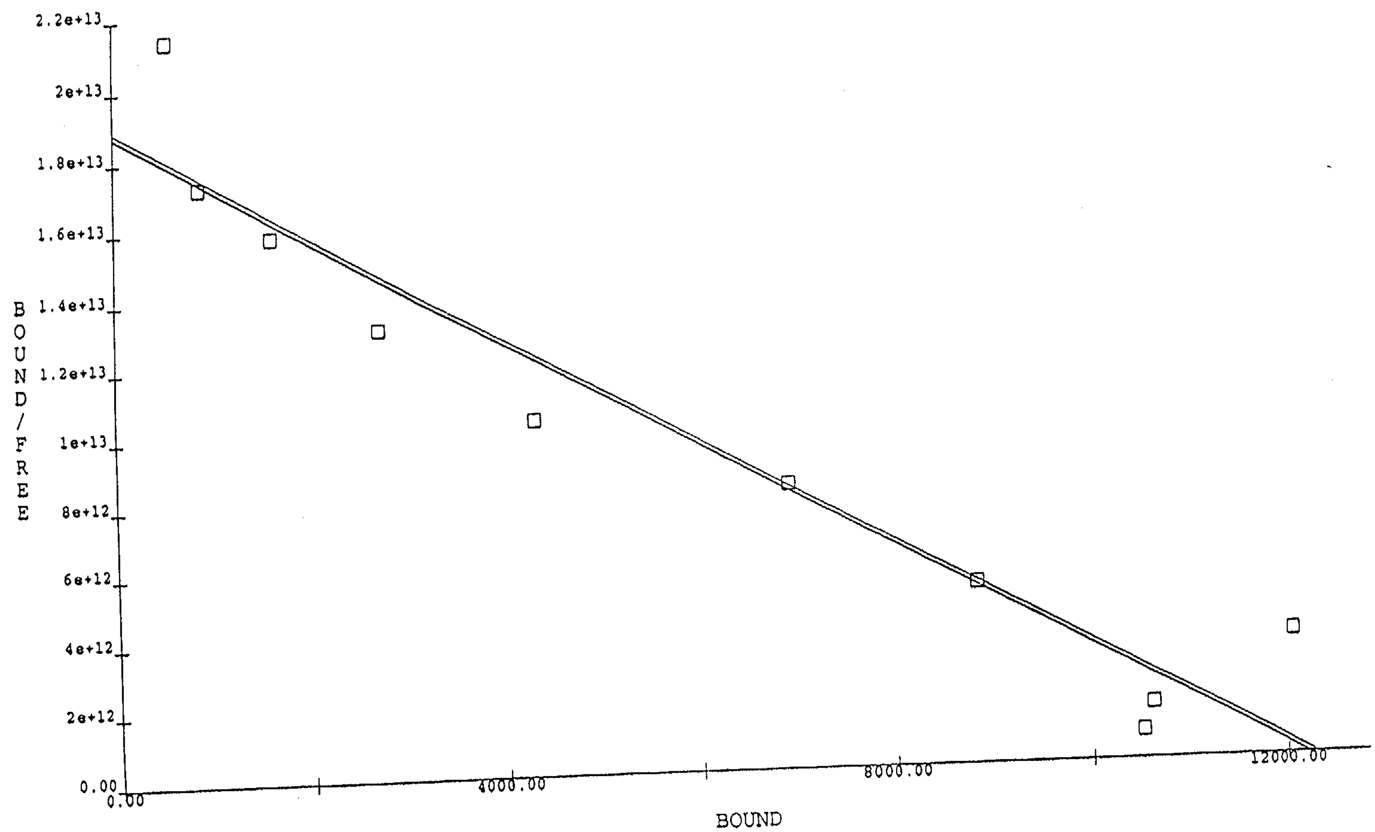
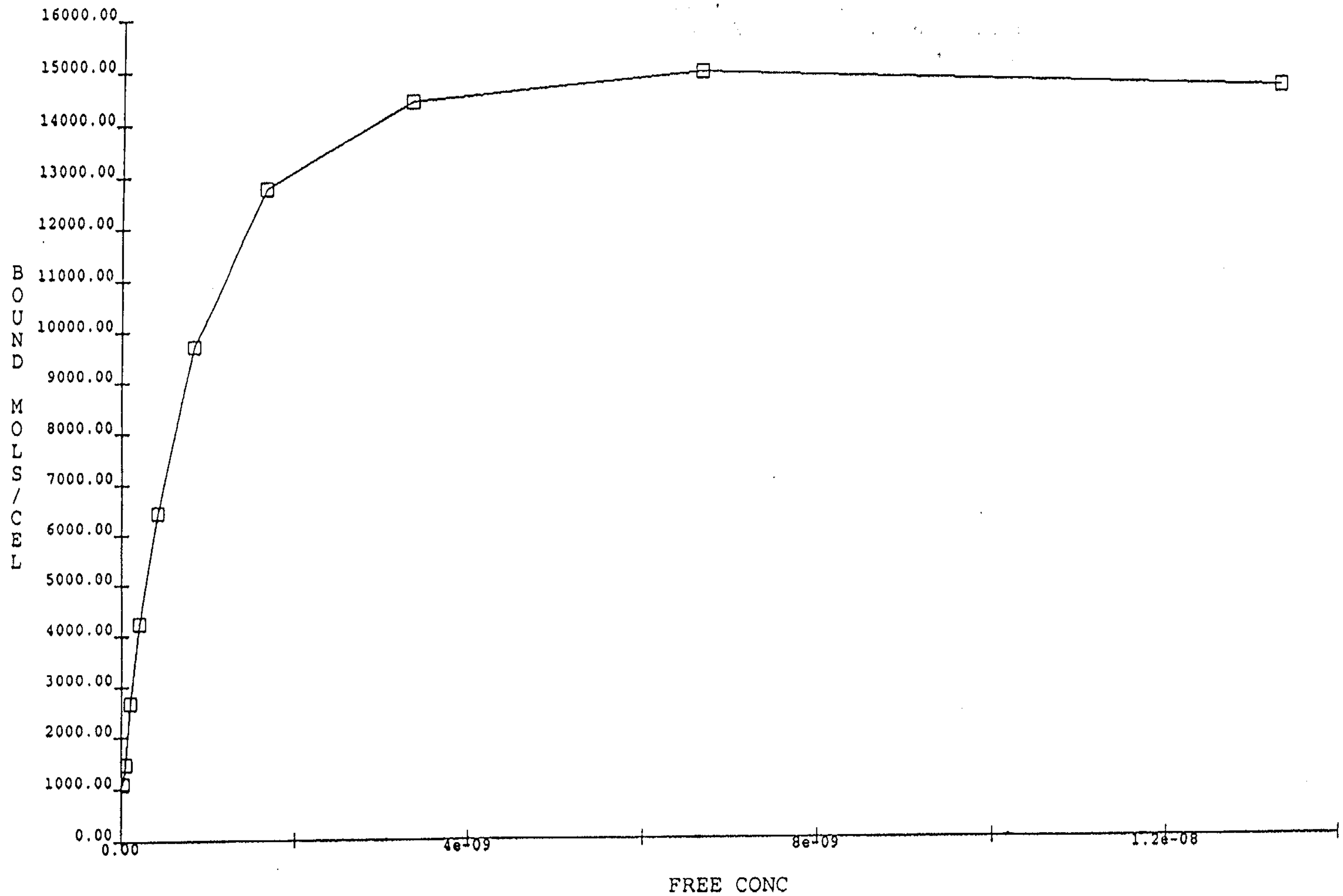

2.2e+13
2e+13
1.8e+13
1.6e+13
1.4e+13
1.2e+13
1e+13
8e+12
6e+12
4e+12
2e+12
0.00
BOUND/FREE
0.00
4000.00
8000.00
12000.00
BOUND

Figure 4B



BOUND MOLS/CEL
16000.00
15000.00
14000.00
13000.00
12000.00
11000.00
10000.00
9000.00
8000.00
7000.00
6000.00
5000.00
4000.00
3000.00
2000.00
1000.00
0.00
0.00
4e-09
8e-09
1.2e-08
FREE CONC

Figure 5A

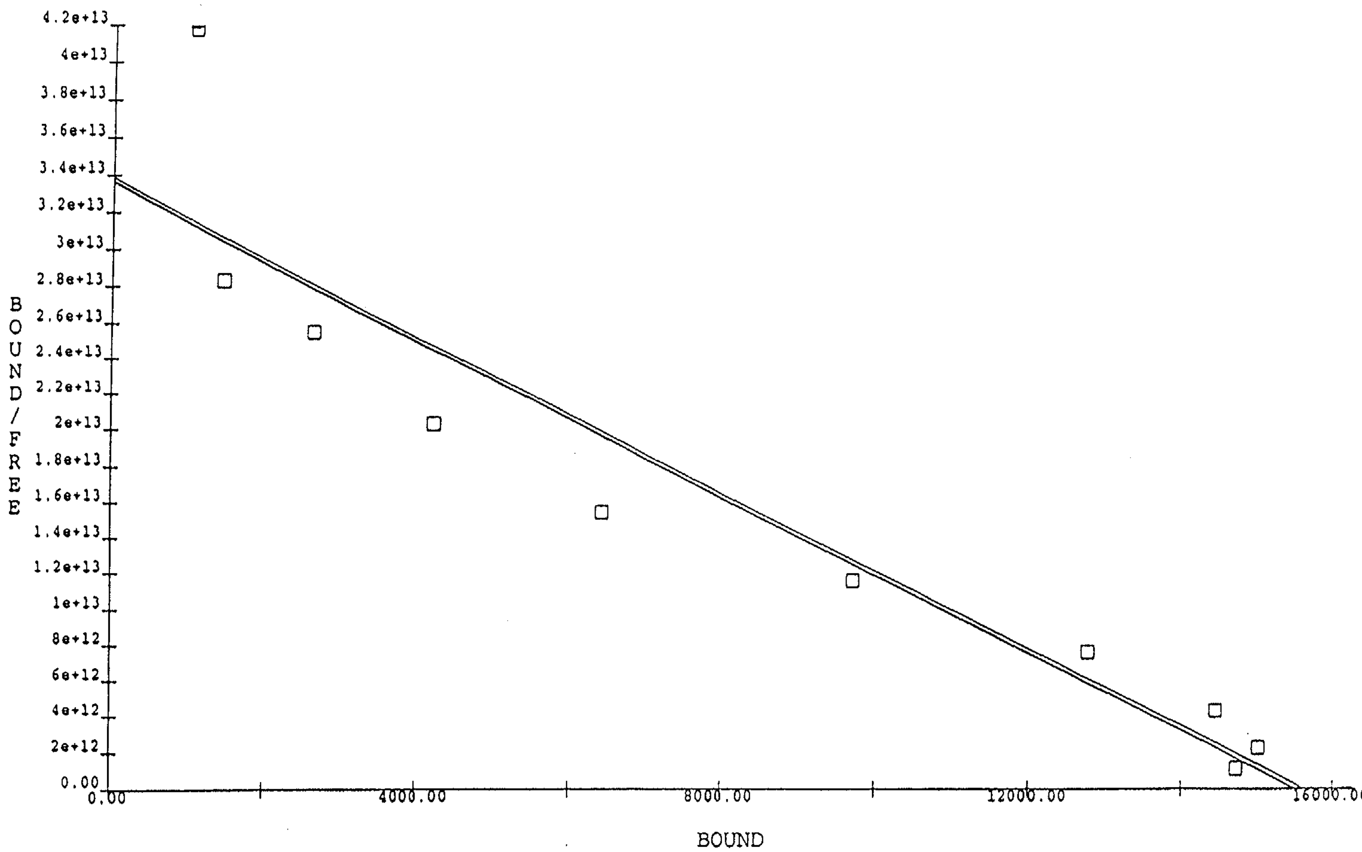

4.2e+13
4e+13
3.8e+13
3.6e+13
3.4e+13
3.2e+13
3e+13
2.8e+13
2.6e+13
2.4e+13
2.2e+13
2e+13
1.8e+13
1.6e+13
1.4e+13
1.2e+13
1e+13
8e+12
6e+12
4e+12
2e+12
0.00
BOUND/FREE
0.00
4000.00
8000.00
12000.00
16000.00
BOUND

Figure 5B

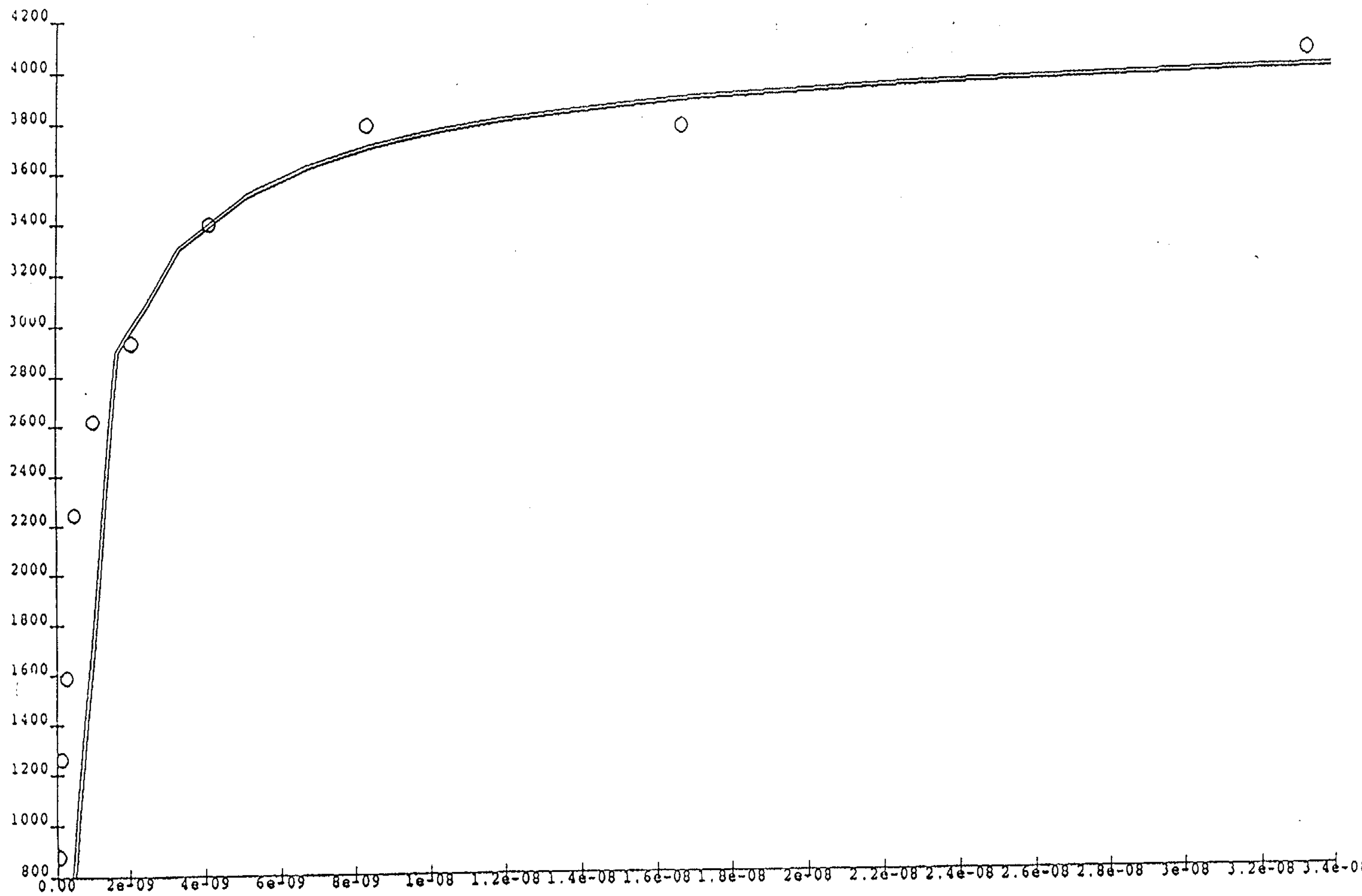

4200
4000
3800
3600
3400
3200
3000
2800
2600
2400
2200
2000
1800
1600
1400
1200
1000
800
0.00
2e-09
4e-09
6e-09
8e-09
1e-08
1.2e-08
1.4e-08
1.6e-08
1.8e-08
2e-08
2.2e-08
2.4e-08
2.6e-08
2.8e-08
3e-08
3.2e-08
3.4e-08
Free Conc (M)

Figure 6A

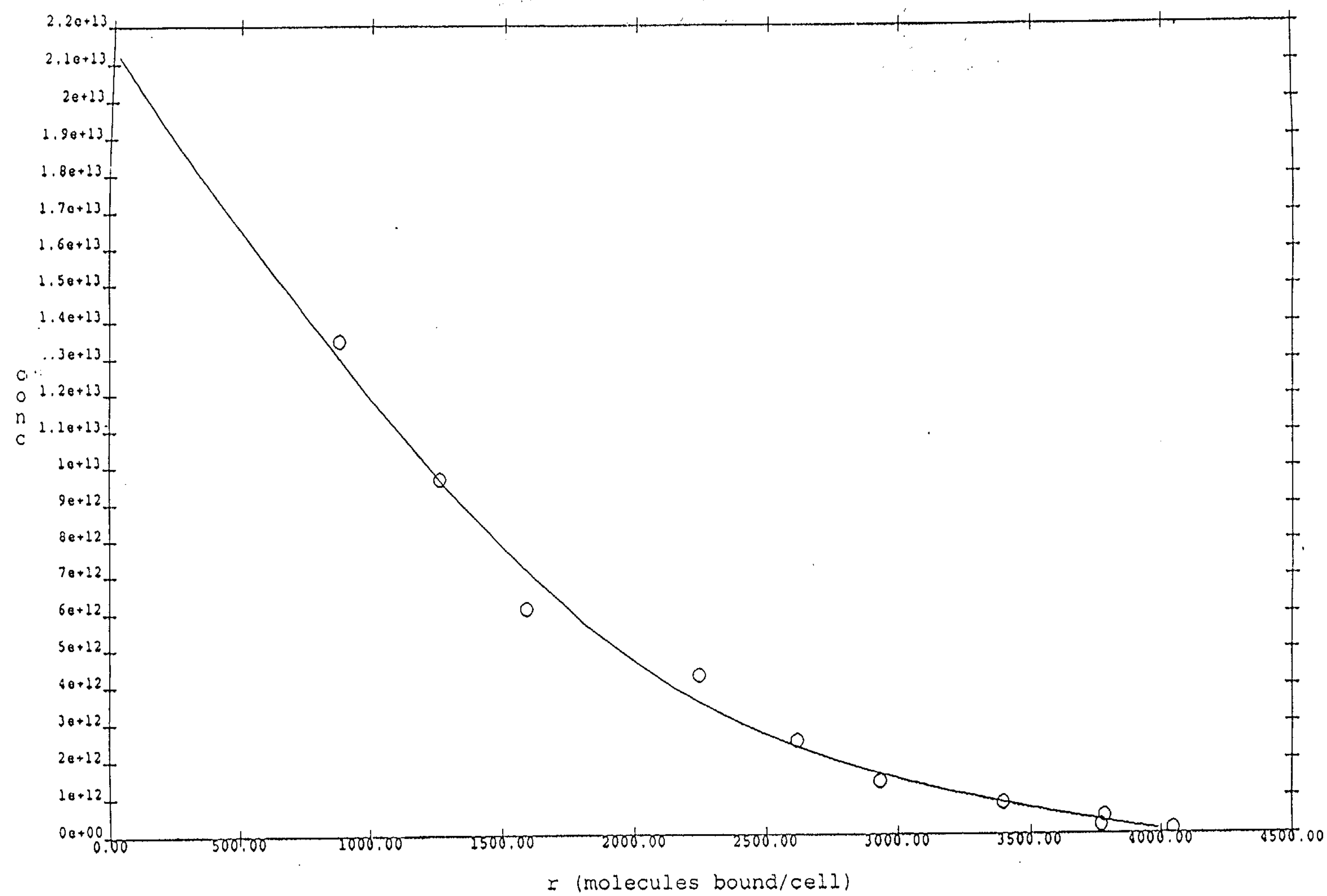

conc
2.2e+13
2.1e+13
2e+13
1.9e+13
1.8e+13
1.7e+13
1.6e+13
1.5e+13
1.4e+13
1.3e+13
1.2e+13
1.1e+13
1e+13
9e+12
8e+12
7e+12
6e+12
5e+12
4e+12
3e+12
2e+12
1e+12
0e+00
0.00
500.00
1000.00
1500.00
2000.00
2500.00
3000.00
3500.00
4000.00
4500.00
r (molecules bound/cell)

Figure 6B